

NA

1643

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# RAW SEQUENCE LISTING

## PATENT APPLICATION US/09/428,122

 DATE: 02/24/2000  
 TIME: 16:25:32

Input Set: I428122.RAW

This Raw Listing contains the General Information  
 Section and up to first 5 pages.

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1 <110> APPLICANT: Connaught Laboratories Limited  
 2 Murdin et al.  
 3 <120> TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND  
 4 USES THEREOF  
 5 <130> FILE REFERENCE: 19721-007-019  
 6 <140> CURRENT APPLICATION NUMBER: US/09/428,122  
 7 <141> CURRENT FILING DATE: 1999-10-27  
 8 <150> EARLIER APPLICATION NUMBER: 60/106,046  
 9 <151> EARLIER FILING DATE: 1998-10-28  
 10 <150> EARLIER APPLICATION NUMBER: 60/132,271  
 11 <151> EARLIER FILING DATE: 1999-05-03  
 12 <160> NUMBER OF SEQ ID NOS: 4  
 13 <170> SOFTWARE: PatentIn Ver. 2.0  
 14 <210> SEQ ID NO 1  
 15 <211> LENGTH: 3000  
 16 <212> TYPE: DNA  
 17 <213> ORGANISM: Chlamydia pneumoniae  
 18 <220> FEATURE:  
 19 <221> NAME/KEY: CDS  
 20 <222> LOCATION: (101)..(2884)  
 21 <400> SEQUENCE: 1

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 24 Met Lys Ser Ser Phe  
 25 1 5  
 26 ccc aag ttt gta ttt tct aca ttt gct att ttc cct ttg tct atg att 163  
 27 Pro Lys Phe Val Phe Ser Thr Phe Ala Ile Phe Pro Leu Ser Met Ile  
 28 10 15 20  
 29 gct acc gag aca gtt ttg gat tca agt gcg agt ttc gat ggg aat aaa 211  
 30 Ala Thr Glu Thr Val Leu Asp Ser Ser Ala Ser Phe Asp Gly Asn Lys  
 31 25 30 35  
 32 aat ggt aat ttt tca gtt cgt gag agt cag gaa gat gct gga act acc 259  
 33 Asn Gly Asn Phe Ser Val Arg Glu Ser Gln Glu Asp Ala Gly Thr Thr  
 34 40 45 50  
 35 tac cta ttt aag gga aat gtc act cta gaa aat att cct gga aca ggc 307  
 36 Tyr Leu Phe Lys Gly Asn Val Thr Leu Glu Asn Ile Pro Gly Thr Gly  
 37 55 60 65  
 38 aca gca atc aca aaa agc tgt ttt aac aac act aag ggc gat ttg act 355  
 39 Thr Ala Ile Thr Lys Ser Cys Phe Asn Asn Thr Lys Gly Asp Leu Thr  
 40 70 75 80 85  
 41 ttc aca ggt aac ggg aac tct cta ttg ttc caa acg gtg gat gca ggg 403  
 42 Phe Thr Gly Asn Gly Asn Ser Leu Leu Phe Gln Thr Val Asp Ala Gly  
 43 90 95 100  
 44 act gta gca ggg gct gct gtt aac agc agc gtg gta gat aaa tct acc 451

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63	Ala Ile Gln Thr Ser Asp Ala Leu Thr Ile Thr Gly Asn Gln Gly Glu	
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66	Val Ser Phe Ser Asp Asn Thr Ser Ser Asp Ser Gly Ala Ala Ile Phe	
67		215 220 225
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86	ggt gga gcc ata gct atc gaa gat agt ggg gaa ttg agt tta tcc gcc	1123
87	Gly Gly Ala Ile Ala Ile Glu Asp Ser Gly Glu Leu Ser Leu Ser Ala	
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89	gat agt ggt gac att gtc ttt tta ggg aat aca gtc act tct act act	1171
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92	cct ggg acg aat aga agt agt atc gac tta gga acg agt gca aag atg	1219
93	Pro Gly Thr Asn Arg Ser Ser Ile Asp Leu Gly Thr Ser Ala Lys Met	
94		360 365 370

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101	gag act ccg gca gat tct gca cta caa tat aca ggg aac atc atc ttc	1363
102	Glu Thr Pro Ala Asp Ser Ala Leu Gln Tyr Thr Gly Asn Ile Ile Phe	
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106	425 430 435	
107	act tcg aag cta cta cag cct gta act ctt tca gga ggt act cta tct	1459
108	Thr Ser Lys Leu Leu Gln Pro Val Thr Leu Ser Gly Gly Thr Leu Ser	
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110	tta aaa cat gga gtg act ctg cag act cag gca ttc act caa cag gca	1507
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113	gat tct cgt ctc gaa atg gac gta gga act act cta gaa cct gct gat	1555
114	Asp Ser Arg Leu Glu Met Asp Val Gly Thr Thr Leu Glu Pro Ala Asp	
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122	tta tct gga acc atc act tta ttg gac ccg acg ggc acg ttt tat gaa	1699
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125	aat cat agt tta aga aat cct cag tcc tac gac atc tta gag ctc aaa	1747
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132	Gly Glu Lys Phe His Tyr Gly Tyr Gln Gly Thr Trp Gly Pro Ile Val	
133	570 575 580	
134	tgg ggg aca ggg gct tct acg act gca acc ttc aac tgg act aaa act	1891
135	Trp Gly Thr Gly Ala Ser Thr Thr Ala Thr Phe Asn Trp Thr Lys Thr	
136	585 590 595	
137	ggc tat att cct aat ccc gag cgt atc ggc tct tta gtc cct aat agc	1939
138	Gly Tyr Ile Pro Asn Pro Glu Arg Ile Gly Ser Leu Val Pro Asn Ser	
139	600 605 610	
140	tta tgg aat gca ttt ata gat att agc tct ctc cat tat ctt atg gag	1987
141	Leu Trp Asn Ala Phe Ile Asp Ile Ser Ser Leu His Tyr Leu Met Glu	
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144	Thr Ala Asn Glu Gly Leu Gln Gly Asp Arg Ala Phe Trp Cys Ala Gly	

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149	cgc cat ttg agt ggc ggt tat gtc ata gga gga aac cta cat act tgt				2131
150	Arg His Leu Ser Gly Gly Tyr Val Ile Gly Gly Asn Leu His Thr Cys				
151		665	670	675	
152	tca gat aag att ctt agt gct gca ttt tgt cag ctc ttt gga aga gat				2179
153	Ser Asp Lys Ile Leu Ser Ala Ala Phe Cys Gln Leu Phe Gly Arg Asp				
154		680	685	690	
155	aga gac tac ttt gta gct aag aat caa ggt aca gtc tac gga gga act				2227
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158	ctc tat tac cag cac aac gaa acc tat atc tct ctt cct tgc aaa cta				2275
159	Leu Tyr Tyr Gln His Asn Glu Thr Tyr Ile Ser Leu Pro Cys Lys Leu				
160		710	715	720	725
161	cgg cct tgt tgc ttg tct tat gtt cct aca gag att cct gtt ctc ttt				2323
162	Arg Pro Cys Ser Leu Ser Tyr Val Pro Thr Glu Ile Pro Val Leu Phe				
163		730	735	740	
164	tca gga aac ctt agc tac acc cat acg gat aac gat ctg aaa acc aag				2371
165	Ser Gly Asn Leu Ser Tyr Thr His Thr Asp Asn Asp Leu Lys Thr Lys				
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167	tat aca aca tat cct act gtt aaa gga agc tgg ggg aat gat agt ttc				2419
168	Tyr Thr Thr Tyr Pro Thr Val Lys Gly Ser Trp Gly Asn Asp Ser Phe				
169		760	765	770	
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171	Ala Leu Glu Phe Gly Gly Arg Ala Pro Ile Cys Leu Asp Glu Ser Ala				
172		775	780	785	
173	cta ttt gag cag tac atg ccc ttc atg aaa ttg cag ttt gtc tat gca				2515
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176	cat cag gaa ggt ttt aaa gaa cag gga aca gaa gct cgt gaa ttt gga				2563
177	His Gln Glu Gly Phe Lys Glu Gln Gly Thr Glu Ala Arg Glu Phe Gly				
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179	agt agc cgt ctt gtg aat ctt gcc tta cct atc ggg atc cga ttt gat				2611
180	Ser Ser Arg Leu Val Asn Leu Ala Leu Pro Ile Gly Ile Arg Phe Asp				
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182	aag gaa tca gac tgc caa gat gca acg tac aat cta act ctt ggt tat				2659
183	Lys Glu Ser Asp Cys Gln Asp Ala Thr Tyr Asn Leu Thr Leu Gly Tyr				
184		840	845	850	
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186	Thr Val Asp Leu Val Arg Ser Asn Pro Asp Cys Thr Thr Leu Arg				
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188	att agc ggt gat tct tgg aaa acc ttc ggt acg aat ttg gca aga caa				2755
189	Ile Ser Gly Asp Ser Trp Lys Thr Phe Gly Thr Asn Leu Ala Arg Gln				
190		870	875	880	885
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192	Ala Leu Val Leu Arg Ala Gly Asn His Phe Cys Phe Asn Ser Asn Phe				
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198      Tyr Asn Val Asp Leu Gly Ala Lys Tyr Gln Phe
199                      920                      925
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212      35 40 45
213      Asp Ala Gly Thr Thr Tyr Leu Phe Lys Gly Asn Val Thr Leu Glu Asn
214      50 55 60
215      Ile Pro Gly Thr Gly Thr Ala Ile Thr Lys Ser Cys Phe Asn Asn Thr
216      65 70 75 80
217      Lys Gly Asp Leu Thr Phe Thr Gly Asn Gly Asn Ser Leu Leu Phe Gln
218      85 90 95
219      Thr Val Asp Ala Gly Thr Val Ala Gly Ala Ala Val Asn Ser Ser Val
220      100 105 110
221      Val Asp Lys Ser Thr Thr Phe Ile Gly Phe Ser Ser Leu Ser Phe Ile
222      115 120 125
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224      130 135 140
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227      Lys Asn Phe Ser Thr Asp Asn Gly Gly Ala Ile Thr Ala Lys Thr Leu
228      165 170 175
229      Ser Leu Thr Gly Thr Thr Met Ser Ala Leu Phe Ser Glu Asn Thr Ser
230      180 185 190
231      Ser Lys Lys Gly Gly Ala Ile Gln Thr Ser Asp Ala Leu Thr Ile Thr
232      195 200 205
233      Gly Asn Gln Gly Glu Val Ser Phe Ser Asp Asn Thr Ser Ser Asp Ser
234      210 215 220
235      Gly Ala Ala Ile Phe Thr Glu Ala Ser Val Thr Ile Ser Asn Asn Ala
236      225 230 235 240
237      Lys Val Ser Phe Ile Asp Asn Lys Val Thr Gly Ala Ser Ser Ser Thr
238      245 250 255
239      Thr Gly Asp Met Ser Gly Gly Ala Ile Cys Ala Tyr Lys Thr Ser Thr
240      260 265 270
241      Asp Thr Lys Val Thr Leu Thr Gly Asn Gln Met Leu Leu Phe Ser Asn
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